

UID: SEQ ID NO:38 Type: DNA 1267 bp  
SEQ ID NO:38

vs.

UID: Jacobs et. al. Type: DNA 481 bp  
Jacobs et. al.

```
Local similarity
Match: 19
Mismatch: -17
Indel start: -13
Indel extend: -7
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Score: 8776 at (SEQ ID NO:38) [456..951] : (Jacobs et. al.) [1..481]

Arrow indicates polynucleotide encoding the C-terminal 15 amino acids of SEQ ID NO:83.

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456 GCAT---GCCGACAAGGCGCGTGGCC-AGCAGAACTGGTGCTGGTTCACATCAGGACAG
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 
1  GAATTCGGCC-A-AA-----GAGGCCTA---AACTGGTGCTGGTTCACATCAGGACAG

```

TGA = STOP codon for SEQ ID NO:83

512 CAACGGGATTCTTTGCTTGTAAAATGTTGCAGTCCACCTGTCCAACTTGATCTTCCGGAA  
|||||||  
50 CAACGGGATTCTTTGCTTGTAAAATGTTGCAGTCCACCTGTCCAACTTGATCTTCCGGAA

632 TGGTCAATCTCAAGCTGGCCACTATCTAGCTATGACCACGTTGCTCTGGAGATGAGCA  
|||||||  
170 TGGTCAATCTCAAGCTGGCCACTATCTAGCTATGACCACGTTGCTCTGGAGATGAGCA

692 CGCCCTTACCTCGCTTCTGGATGCTCTAAAGGCGGGCTGGTCCGAGTCTCTGTTT  
|||  
230 CGCCCTTACCTCGCTTCTGGATGCTCTAAAGGCGGGCTGGTCCGAGTCTCTGTTT

752 GGAAGCTCAACCACTGGCTGATGATTCACATGTTCACTGCCGATGGTTCTAACCTTACCC  
290 GGAAGCTCAACCACTGGCTGATGATTCACATGTTCACTGCCGATGGTTCTAACCTTACCC

812 ACATGTGGTGGGTGTGTTCTGGCACTGGGACGGCCTGGTCAGCAGCCTGTATCTGCCCTC  
|||||||  
350 ACATGTGGTGGGTGTGTTCTGGCACTGGGACGGCCTGGTCAGCAGCCTGTATCTGCCCTC

872 ATTTGACACTGTTCTTGTGCGACTGGCTCTGCTTACGCTAATCTTAAATCCATATTGGAA  
410 ATTTGACACTGTTCTTGTGCGACTGGCTCTGCTTACGCTAATCTTAAATCCATATTGGAA

932 CCCATAAGAAGACTCAGCAG  
470 CCC-----AGACTC-G-AG

Percent Identity: 95.0  
Percent Similarity: 95.0